



OIPE

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/844,684

DATE: 01/26/2002

TIME: 16:16:22

Input Set : A:\Sequence Listing.asc

Output Set: N:\CRF3\01262002\I844684.raw

**Does Not Comply**  
**Corrected Diskette Needed**

5 <110> APPLICANT: GEMINI SCIENCE, INC.  
 6 LA JOLLA INSTITUTE FOR ALLERGY AND IMMUNOLOGY  
 8 <120> TITLE OF INVENTION: HUMAN ANTI-CD40 ANTIBODIES AND METHODS OF MAKING SAME  
 10 <130> FILE REFERENCE: 21286/0276339  
 12 <140> CURRENT APPLICATION NUMBER: US 09/844,684  
 13 <141> CURRENT FILING DATE: 2001-04-27  
 15 <150> PRIOR APPLICATION NUMBER: US 60/200,601  
 16 <151> PRIOR FILING DATE: 2000-04-28  
 18 <160> NUMBER OF SEQ ID NOS: 15  
 20 <170> SOFTWARE: PatentIn Ver. 2.1

## ERRORED SEQUENCES

22 <210> SEQ ID NO: 1  
 23 <211> LENGTH: 40  
 24 <212> TYPE: DNA  
 25 <213> ORGANISM: Artificial Sequence  
 27 <220> FEATURE:  
 28 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer  
 30 <400> SEQUENCE: 1  
 E--> 31 cccagatctg tccatccaga accaccact gcatgcagag *40 format error*  
 32 40  
 35 <210> SEQ ID NO: 2  
 36 <211> LENGTH: 41  
 37 <212> TYPE: DNA  
 38 <213> ORGANISM: Artificial Sequence  
 40 <220> FEATURE:  
 41 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer  
 43 <400> SEQUENCE: 2  
 E--> 44 acaagatctg ggctctacgt atctcagccg atcctgggga c *same error*  
 45 41  
 48 <210> SEQ ID NO: 3  
 49 <211> LENGTH: 26  
 50 <212> TYPE: DNA  
 51 <213> ORGANISM: Artificial Sequence  
 53 <220> FEATURE:  
 54 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer  
 56 <400> SEQUENCE: 3  
 E--> 57 gtgcacgccg ctggtcaggg cgcttg *same*  
 58 26  
 61 <210> SEQ ID NO: 4  
 62 <211> LENGTH: 26

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63 <212> TYPE: DNA  
64 <213> ORGANISM: Artificial Sequence  
W--> 65 <220> FEATURE:  
66 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer *same*  
68 <400> SEQUENCE: 4  
E--> 69 gttgaagctc tttgtgacgg gcgagc  
70 26  
73 <210> SEQ ID NO: 5  
74 <211> LENGTH: 30  
75 <212> TYPE: DNA  
76 <213> ORGANISM: Artificial Sequence  
78 <220> FEATURE:  
79 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer  
81 <400> SEQUENCE: 5  
E--> 82 accgtgtcga cggtgatcag gactgaacag  
83 30  
86 <210> SEQ ID NO: 6  
87 <211> LENGTH: 29  
88 <212> TYPE: DNA  
89 <213> ORGANISM: Artificial Sequence  
91 <220> FEATURE:  
92 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer  
94 <400> SEQUENCE: 6  
E--> 95 accgtgtcga cgctgatcag gactgcaca  
96 29  
99 <210> SEQ ID NO: 7  
100 <211> LENGTH: 24  
101 <212> TYPE: DNA  
102 <213> ORGANISM: Artificial Sequence  
104 <220> FEATURE:  
105 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer  
107 <400> SEQUENCE: 7  
E--> 108 agtgctagct gaggagacgg tgac  
109 24  
112 <210> SEQ ID NO: 8  
113 <211> LENGTH: 30  
114 <212> TYPE: DNA  
115 <213> ORGANISM: Artificial Sequence  
117 <220> FEATURE:  
118 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer  
121 <400> SEQUENCE: 8  
E--> 122 aactccagat ctagggcaag cagtggtaac  
123 30  
126 <210> SEQ ID NO: 9  
127 <211> LENGTH: 30  
128 <212> TYPE: DNA  
129 <213> ORGANISM: Artificial Sequence  
131 <220> FEATURE:  
132 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer

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134 <400> SEQUENCE: 9  
E--> 135 tatccccgtac ggttgatctc caccttggtc  
136 30  
139 <210> SEQ ID NO: 10  
140 <211> LENGTH: 520  
141 <212> TYPE: DNA  
142 <213> ORGANISM: Homo sapiens  
144 <400> SEQUENCE: 10  
E--> 145 gctgatcagg actgcacaca gagaactcac catggagttt gggctgagct  
146 gggttttcct 60  
E--> 147 tgttgctatt ttaaaagggtg tccagtgtga ggtgcagctg gtggagtccg  
148 ggggaggctt 120  
E--> 149 agttcagcct ggggggtccc tgagactctc ctgtgcagtc tctggattca  
150 ccttcagtag 180  
E--> 151 ctactggatg cactgggtcc gccaaagctcc aggggaagggg ctggtgtggg  
152 tctcacgtat 240  
E--> 153 taatagtgat gggagtagca caacctacgc ggactccgtg aagggccgat  
154 tcaccatctc 300  
E--> 155 cagagacaac gccaaagaaca cgctgtatct gcaaataaac agtctgagag  
156 ccgaggacac 360  
E--> 157 ggctgtgtat tactgtgcaa gagatagagt actatggatc ggggagttat  
158 cctactacgg 420  
E--> 159 tatggacgtc tggggccaag ggaccacggt caccgtctcc tcagctagca  
160 ccaagggccc 480  
E--> 161 atcgggtcttc cccctggcac cctcctccaa gagcacctct  
162 520  
165 <210> SEQ ID NO: 11  
166 <211> LENGTH: 698  
167 <212> TYPE: DNA  
168 <213> ORGANISM: Homo sapiens  
170 <400> SEQUENCE: 11  
E--> 171 ggggagtcag acccagtcag gacacagcat ggacatgagg gtccccgctc  
172 agctcctggg 60  
E--> 173 gctcctgctg ctctggctcc caggtgccaa atgtgacatc cagatgaccc  
174 agtctccttc 120  
E--> 175 caccctgtct gcatctgtag gagacagagt caccatcact tgccgggcca  
176 gtcagagtat 180  
E--> 177 tagtaactgg ttggcctggt atcagcagaa accagggaaa gccctaagc  
178 tctgtctcta 240  
E--> 179 taaggcatct ggtttagaaa gtgggggtccc atcaaggttc agcggcagtg  
180 gatctgggac 300  
E--> 181 agaattcact ctccacctca acagcctgca gcctgatgat tttgcaactt  
182 attactgcca 360  
E--> 183 acagtctaag agttattcgt ggacgttcgg ccacgggacc aagggtgaaa  
184 tcaaactgtac 420  
E--> 185 ggtggctgca ccactgtctc tcactctccc gccatctgat gagcagttga  
186 aatctggaac 480  
E--> 187 tgcctctgtt gtgtgcctgc tgaataactt ctatcccaga gaggccaaag  
188 tacagtggaa 540

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E--> 189 ggtggataac gccctccaat cgggtaactc ccaggagagt gtcacagagc  
190 aggacagcaa 600

E--> 191 ggacagcacc tacagcctca gcagcaccct gacgctgagc aaagcagact  
192 acgagaaaca 660

E--> 193 caaagtctac gcctgcgaag tcacccatca gggcctga  
194 698  
197 <210> SEQ ID NO: 12  
198 <211> LENGTH: 580  
199 <212> TYPE: DNA  
200 <213> ORGANISM: Homo sapiens  
202 <400> SEQUENCE: 12

E--> 203 ggtgatcagg actgaacagg gagaactcac catggagttt gggctgggct  
204 ggctttttct 60

E--> 205 tgtggctatt ttaaaagggtg tccagtgtga ggtgcagctg ttggagtctg  
206 ggggaggctt 120

E--> 207 ggtacagcct ggggggtccc tgagactctc ctgtgcagcc tctggattcg  
208 ccttttagcag 180

E--> 209 ctatgccatg agctgggtcc gccaggctcc aggggaagggg ctggagtggg  
210 tctcagctat 240

E--> 211 tagtggtagt ggtggtagca catactacgc agactccgtg aagggccggt  
212 tcacccatctc 300

E--> 213 cagagacaat tccaagaaca cgctgtatct gcaaatgaac agcctgagag  
214 ccgaggacac 360

E--> 215 ggccgtatat tactgtgcga aagatggggg gtactatggt tcggggagtt  
216 atgggtactt 420

E--> 217 tgactactgg ggccaggga cctgtgtcac cgtctctca gctagcacca  
218 agggcccatc 480

E--> 219 ggtcttcccc ctggcaccct cctccaagag cactcttggg ggcacagcgg  
220 cctgggctg 540

E--> 221 cctgggtcaag gactacttcc ccgaaccggt gacggtgtcg  
222 580  
226 <210> SEQ ID NO: 13  
227 <211> LENGTH: 716  
228 <212> TYPE: DNA  
229 <213> ORGANISM: Homo sapiens  
231 <400> SEQUENCE: 13

E--> 232 caacgcagag tacgcgggga ggagtcagac ccagtcagga cacagcatgg  
233 acatgagggt 60

E--> 234 ccccgctcag ctccctggggc tcctgtgtct ctggttccca ggttccagat  
235 gcgacatcca 120

E--> 236 gatgaccag tctccatctt ccgtgtctgc atctgcagga gacagagtca  
237 ccatcacttg 180

E--> 238 tcgggcgagt cagggtatta gcagctggtt agcctggtat caacagaaac  
239 cagggaagc 240

E--> 240 ccctaagctc ctgatctatg ctggatccag tttgcaaagt ggggtcccat  
241 caaggttcag 300

E--> 242 cggcagtgga tttgggacag atttactct caccatcggc agcctgcagc  
243 ctgaagattt 360

E--> 244 tgcaacttac tattgtcaac aggctagcag tttccctcgg acgttcggcc

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```

      245 aagggaccaa 420
E--> 246 ggtggagatc aaacgtacgg tggetgcacc atctgtcttc atcttcccgc
      247 catctgatga 480
E--> 248 gcagttgaaa tctggaactg cctctgttgt gtgcctgctg aataacttct
      249 atcccagaga 540
E--> 250 ggccaaagta cagtgggaagg tggataacgc cctccaatcg ggtaactccc
      251 aggagagtgt 600
E--> 252 cacagagcag gacagcaagg acagcaccta cagcctcage agcacctga
      253 cgctgagcaa 660
E--> 254 agcagactac gagaaacaca aagtctacgc ctgcgaagtc acccatcagg gcctga
      255 716
      258 <210> SEQ ID NO: 14
      259 <211> LENGTH: 630
      260 <212> TYPE: DNA
      261 <213> ORGANISM: Homo sapiens
      263 <400> SEQUENCE: 14
E--> 264 ggtctatata agcagagctg ggtacgtcct cacattcagt gatcagcact
      265 gaacacagac 60
E--> 266 ccgtcgacgg tgatcaggac tgaacagaga gaactcacca tggagtttgg
      267 gctgagctgg 120
E--> 268 ctttttcttg tggctatattt aaaaggtgtc cagtgtgagg tgcagctgtt
      269 ggagtctggg 180
E--> 270 ggaggcttgg tacagcctgg ggggtccctg agactctcct gtgcagcctc
      271 tggattcacc 240
E--> 272 tttagcagct atgccatgag ctgggtccgc caggctccag ggaaggggct
      273 ggagtgggtc 300
E--> 274 tcagctatta gtggtagtgg tggtagcaca tactacgcag actccgtgaa
      275 gggccgggtc 360
E--> 276 accatctcca gagacaattc caagaacacg ctgtatctgc aatgaacag
      277 cctgagagcc 420
E--> 278 gaggacacgg ccgtatatata ctgtgcgaaa gatgggggggt actatgggtc
      279 ggggagttat 480
E--> 280 gggtaacttg actactgggg ccagggaacc ctggtcaccg tctcctcage
      281 tagcaccaag 540
E--> 282 ggcccatcgg tcttccccct ggcaccctcc tccaagagca cctctggggg
      283 cacagcggcc 600
E--> 284 ctgggctgcc tggteaagga ctacttcccc
      285 630
      288 <210> SEQ ID NO: 15
      289 <211> LENGTH: 728
      290 <212> TYPE: DNA
      291 <213> ORGANISM: Homo sapiens
      293 <400> SEQUENCE: 15
E--> 294 caagcagtgg taacaacgca gagtacgcgg ggggagtcag acccagtcag
      295 gacacagcat 60
E--> 296 ggacatgagg gtccccgctc agctcctggg gctcctgctg ctctgggtcc
      297 caggttccag 120
E--> 298 atgcgacatc cagatgaccc agtctccatc ttccgtgtct ggatctgtag
      299 gagacagagt 180

```

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E--> 300 caccatcact tgtcgggcga gtcagggtat tagcagctgg ttagcctggt  
301 atcagcagaa 240  
E--> 302 accagggaaa gcccctaagc tcctgatcta tgctggatcc agtttgcaaa  
303 gtgggggtccc 300  
E--> 304 atcaagggtc agcggcagtg gatttgggac agatttcact ctcaccatca  
305 gcagcctgca 360  
E--> 306 gcctgaagat tttgcaactt actattgtca acaggctagc agtttcctc  
307 ggacattcgg 420  
E--> 308 ccaaggagacc aagggtggaga tcaaacgtac ggtggctgca ccattctgtct  
309 tcattcttccc 480  
E--> 310 gccatctgat gacgagttga aatctggaac tgctctgtt gtgtgctgc  
311 tgaataactt 540  
E--> 312 ctatcccaga gaggccaaag tacagtggaa ggtggataac gccctccaat  
313 cgggtaactc 600  
E--> 314 ccaggagagt gtcacagagc aggacagcaa ggacagcacc tacagcctca  
315 gcagcaccct 660  
E--> 316 gacgctgagc aaagcagact acgagaaaca caaagtctac gcctgcgaag  
317 tcacccatca 720  
E--> 318 gggcctga  
319 728



## VERIFICATION SUMMARY

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Input Set : A:\Sequence Listing.asc

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L:31 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:40 SEQ:1  
L:44 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:41 SEQ:2  
L:57 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:26 SEQ:3  
L:65 M:283 W: Missing Blank Line separator, <220> field identifier  
L:69 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:26 SEQ:4  
L:82 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:30 SEQ:5  
L:95 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:29 SEQ:6  
L:108 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:24 SEQ:7  
L:122 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:30 SEQ:8  
L:135 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:30 SEQ:9  
L:145 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:10  
M:254 Repeated in SeqNo=10  
L:171 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:11  
M:254 Repeated in SeqNo=11  
L:203 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:12  
M:254 Repeated in SeqNo=12  
L:232 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:13  
M:254 Repeated in SeqNo=13  
L:264 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:14  
M:254 Repeated in SeqNo=14  
L:294 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:15  
M:254 Repeated in SeqNo=15